

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:23:48 ; Search time 48.0429 Seconds
(without alignments)
102.055 Million cell updates/sec

Title: US-09-905-691-2

Perfect score: 19

Sequence: 1 ARAARRAARRAARRAEEA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTRMBL_23:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rrodent:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_virus:
 16: sp_bacteriap:
 17: sp_archeap:

091481 pseudomonas

Q8s112 oryza sativ

091211 streptomyce

Q965y4 caenorhabdi

Q8ft37 corynebacte

Q8xq3 neurospora

Q8yer0 brucella me

Q98cc1 rhizobium l

060961 leishmania

Q9s2k3 streptomyce

Q942t3 oryza sativ

08yub7 anaerbaena sp

Q8u8g2 agrobacteri

Q8z368 salmonella

Q94n10 Plauricospo

Q8kb54 chlorobiolum

08f1j3 escherichia

011376 molluscum c

Q98316 molluscum c

Q8h286 ananas como

Q94n10 Plauricospo

Q8kb54 chlorobiolum

08p9a4 xanthomonas

Q8n9d2 homo sapien

Q8w322 oryza sativ

Q95bp0 pleuricospo

Q910cl pseudomonas

Q8nh35 homo sapien

Q8nh35 homo sapien

Q943b9 oryza sativ

Q9a3r0 caulobacter

Q8lh12 oryza sativ

ALIGNMENTS

RESULT 1
Q94ev7
ID 094ev7
AC Q94ev7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE MAP kinase kinase.
GN MAPKK.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophytta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCDI clade; Panicoideae; NCBI_TaxID=4577;
OX RN [1]
RN SEQUENCE FROM N.A.
RC SPERMATOPHYZA-Husk2;
RA FU H.; Zheng Z.; Dooner H.K.;
RT "Large differences in recombination rates within adjacent gene-dense
and retrotransposon regions of maize.";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC 1-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AF391808; AAC73104.1;
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002965; P_rich_extensin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
PFam; PF00669; pkinase; 1.
PRINTS; PRO12177; PRICHEPTENSN.
PRINTS; PRO00109; TYRKINASE.
DR PROSITE; PS00001; Prot_kinase; 1.
DR SMART; SM00226; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 406 AA; 4464 MW; DBP1DE6568F4 DF0 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	10	52.6	406	10	Q94ev7	09lev7 zea mays (m	
2	9	47.4	105	2	P96802	P96802 mycobacteri	
3	9	47.4	105	16	Q9CC08	Q9ccq8 mycobacteri	
4	9	47.4	190	16	P71658	P71658 mycobacteri	
5	9	47.4	750	16	Q9KRP6	Q9krp6 streptomyce	
6	8	42.1	101	11	Q8Bav6	Q8bmv6 mus musculu	
7	8	42.1	127	2	Q8G161	Q8g161 terrabacter	
8	8	42.1	144	17	Q9YD73	Q9yd73 aeropyrum p	
9	8	42.1	167	10	Q8SSU9	Q8s1j9 oryza sativ	
10	8	42.1	204	12	Q9X696	Q9x696 streptomyce	
11	8	42.1	204	12	Q65545	Q65545 bovine harp	
12	8	42.1	274	10	Q8G2B4	Q9ze4 Pyrocystis	
13	8	42.1	327	16	Q30370	Q30370 pseudomonas	
14	8	42.1	328	16	Q9II15	Q9ii15 pseudomonas	
15	8	42.1	336	2	Q9X440	Q9x4x0 pseudomonas	
16	8	42.1	356	7	Q31191	Q31191 mus musculu	

Query Match 52.6%; Score 10; DB 10; Length 406;

RL	DNA Res. 6:83-101(1999).	DR	TIGFRAMS; TIGR00421; ub1x; 1.
DR	ENBL; AP000060; BAB80024.1;	SQ	SEQUENCE 200 AA; 21660 MW; 83D1B5C22C13CD3E CRC64;
KW	Hypothetical Protein; Complete Proteome.		
SEQUENCE 144 AA; 14937 MW;	973D6C01A0449375 CRC64;		
SO			
Query Match	42.1%; Score 8; DB 17; Length 144;	Query Match	42.1%; Score 8; DB 2; Length 200;
Best Local Similarity	100.0%; Pred. No. 23;	Best Local Similarity	100.0%; Pred. No. 30;
Matches 8;	Conservative 0; Mismatches 0;	Matches 8;	Conservative 0; Mismatches 0;
Indels 0;	Gaps 0;	Indels 0;	Gaps 0;
Qy	3 AARRAARA 10	Qy	6 RAARRAAR 13
Db	3 AARRAARA 10	Db	187 RAARRAAR 194
RESULT 9		RESULT 11	
QBS1J9	PRELIMINARY;	Q65545	PRELIMINARY;
ID	PRT; 167 AA.	ID	PRT; 204 AA.
AC		AC	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Q65545;	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	P0584C02.19 Protein.	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN	P0584C02.19.	DE	DL3 Protein.
OS	Oryza sativa (Japonica cultivar-group).	GN	UL3.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OS	Bovine herpesvirus 1.
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC	Enharcocidae; Oryzeae; Oryza.	OC	Alpha herpesvirinae; Varicellovirus.
OX	NCBI_TaxID=39947;	OX	NCBI_TaxID=10320;
RN		RN	SEQUENCE FROM N.A.
RP		RP	SPRAIN=Cooper;
RC		RC	RC
SEQUENCE FROM N.A.		SEQUENCE	MEDLINE=9603477; PubMed=7483276;
STRAIN=cv. Nipponbare;		RA	Rikhtar S.K., van Drunen Littel-van den Hurk S., Babiuk L.A.,
RA		RA	Rikoor S.K.;
RT	Sasaki T., Matsumoto T., Yamamoto K.; genomic DNA, chromosome 1, PAC	RT	Identification and transcriptional analysis of a 3'-coterminal gene
RT	clone (p0584C02-1).	RT	cluster containing UL1, UL2, UL3, and UL3.5 open reading frames of
RT	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.	RT	bovine herpesvirus-1.
DR		RL	Virology 213:28-37(1998).
DR	EMBL; AP003290; BAB89063.1;	DR	EMBL; U32173; AAC34557.1;
DR	Gramene; QBS1J9; -.	DR	InterPro; IPR005035; Herpes_UL3.
SQ	SEQUENCE 167 AA; 18542 MW;	DR	InterPro; IPR05849; Sug_transporter.
Qy	0C40040DFB49021B CRC64;	DR	PFam; PF03365; Herpes_DL3.1.
Query Match	42.1%; Score 8; DB 10; Length 167;	DR	PROTEIN: PS00216; SUGAR_TRANSPORT_1.1
Best Local Similarity	100.0%; Pred. No. 26;	SQ	SEQUENCE 204 AA; 21792 MW; 9292E8AA2CB8C6 CRC64;
Matches 8;	Conservative 0; Mismatches 0;	Query Match	42.1%; Score 8; DB 12; Length 204;
Indels 0;	Gaps 0;	Best Local Similarity	100.0%; Pred. No. 31;
Qy	5 RAARRAAA 12	Matches 8;	Matches 0;
Db	20 RAARRAAA 27	Qy	6 RAARRAAR 13
		Db	113 RAARRAAR 120
RESULT 10		RESULT 12	
Q9X696	PRELIMINARY;	Q8GZEA4	PRELIMINARY;
ID	PRT; 200 AA.	ID	PRT; 274 AA.
AC		AC	
Q9X696;		Q8GZEA4;	
DT	01-NOV-1999 (TREMBLrel. 12, Created)	DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	VdCB.	DE	Chlorophyll A-C binding protein.
GN	Streptomyces sp. (strain D7).	OS	Pyrocystis lunula.
OS	Bacteria; Actinobacteria; Actinomycetales;	OC	Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.
OC	Streptomycineae; Streptomyctaceae; Streptomyces.	OX	NCBI_TaxID=2972;
OX	NCBI_TaxID=92742;	RN	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC		RA	Okamoto O.K., Hastings J.W.;
RX	MEDLINE=99445180; PubMed=10517592;	RA	"Circadian oscillations in the transcriptome of dinoflagellate cells:
RA	Chow K.T., Pope M.K., Davies J.;	RT	towards the clock circuitry."
RT	Characterization of a vanillic acid non-oxidative decarboxylation	RT	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RT	gene cluster from Streptomyces sp. D7.";	RL	EMBL; AF0134539; AAD28781.1;
RL	Microbiology 145:2393-2403(1999).	DR	AF508261; AA014680.1;
DR	InterPro; IPR003182; Flavoprotein.	SQ	SEQUENCE 274 AA; 28168 MW; B5F532A5D45AC9BA CRC64;
DR	InterPro; IPR004307; Ub1X.	Query Match	42.1%; Score 8; DB 10; Length 274;
DR	Pfam; PF02441; Flavoprotein; 1.	Best Local Similarity	100.0%; Pred. No. 39;

Qy	10 AAARRARA 17 	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RT "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen."; RT Nature 406:959-964(2000); RL EMBL; AE004651; AAC05642.1; -.
Db	81 AAARRARA 88		KW Complete proteome. SQ SEQUENCE 328 AA; 37134 MW; DEE46CA9BEPF43B29 CRC64;
RESULT 13			Query Match 42.1%; Score 8; DB 16; Length 328;
030370	ID 030370 PRELIMINARY; AC 030370; DT 01-JAN-1998 (TREMBLrel. 05, Created) DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	Best Local Similarity 100.0%; Pred. No. 45; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RT Best Local Similarity 100.0%; Pred. No. 45; RL Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PVCA.	GN OS <i>Pseudomonas aeruginosa</i> . OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; OC Pseudomonadaceae; Pseudomonas . OX NCBI_TAXID=287; RN [1]		
RP SEQUENCE FROM N.A.			RESULT 15
RC STRAIN=PAO1;	RX MEDLINE=96254009; PubMed=8704959;	Q9X4X0 ID Q9X4X0; PRELIMINARY; AC Q9X4X0; DT 01-NOV-1999 (TREMBLrel. 12, Created) DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	Q9X4X0 ID Q9X4X0; PRELIMINARY; AC Q9X4X0; DT 01-NOV-1999 (TREMBLrel. 12, Created) DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
RA Stintzi A., Cornelis P., Hohndel D., Meyer J.M., Dean C., Poole K., RA Kouremans S., Krishnapillai V.,	RA Stintzi A., Johnson Z., Stonehouse M., Ochsner U., Meyer J.M., RA Vasili M.L., Poole K.,	QY 1 ARAARRAA 8 Db 319 ARAARRAA 326	QY 1 ARAARRAA 8 Db 319 ARAARRAA 326
RT Novel Poyeridine biosynthesis gene(s) of <i>Pseudomonas aeruginosa</i> PAO1; RL Microbiology 142:1181-1190(1996).	RT The pvc gene cluster of <i>Pseudomonas aeruginosa</i> : role in synthesis of RL Bacteriophore 181:4118-4124(1999).		
RN [2]	RP SEQUENCE FROM N.A.		
RC STRAIN=PAO1;	RX MEDLINE=9315810; PubMed=10363985;	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Stintzi A., Johnson Z., Stonehouse M., Ochsner U., Meyer J.M., RA Vasili M.L., Poole K.,	RA Stintzi A., Johnson Z., Stonehouse M., Ochsner U., Meyer J.M., RA Vasili M.L., Poole K.,	RC STRAIN=BRME-9; RA Mohr W.W., Wilson A.E., Bicho P., Moore E.R.B.; RT "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin Acids"; RT Syst. Appl. Microbiol. 0:0-0(1999).	RC STRAIN=BRME-9; RA Mohr W.W., Wilson A.E., Bicho P., Moore E.R.B.; RT "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin Acids"; RT Syst. Appl. Microbiol. 0:0-0(1999).
RT The pvc gene cluster of <i>Pseudomonas aeruginosa</i> : role in synthesis of RT Bacteriophage 181:4118-4124(1999).	RT The pvc gene cluster of <i>Pseudomonas aeruginosa</i> : role in synthesis of RT Bacteriophage 181:4118-4124(1999).	RL SEQUENCE FROM N.A.	RL SEQUENCE FROM N.A.
DR EMBL; AF002222; AAC21671.1; -.	DR EMBL; AF002222; AAC21671.1; -.	DR STRAIN=BRME-9; RA Martin V.J., Mohn W.W.; RA Martin V.J., Mohn W.W.;	DR STRAIN=BRME-9; RA Martin V.J., Mohn W.W.;
SQ SEQUENCE 327 AA; 37019 MW; 08286FF3B127C9BB CRC64;	SQ SEQUENCE 327 AA; 37019 MW; 08286FF3B127C9BB CRC64;	DR InterPro; IPR002529; FAA_hydrolase; DR Pfam; PF01557; FAA_hydrolase; 1.	DR InterPro; IPR002529; FAA_hydrolase; DR Pfam; PF01557; FAA_hydrolase; 1.
Query Match 42.1%; Score 8; DB 2; Length 327;	Query Match 42.1%; Score 8; DB 2; Length 327;	SQ SEQUENCE 336 AA; 37494 MW; CD221163FB1B44FB CRC64;	Query Match 42.1%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 45;	Best Local Similarity 100.0%; Pred. No. 45;	Best Local Similarity 100.0%; Pred. No. 46;	Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PVCA OR PA2254.			
OS <i>Pseudomonas aeruginosa</i> .			
OC Pseudomonadaceae; Pseudomonas .			
NCBI_TAXID=287;			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 15692 / PAO1;			
RX MEDLINE=2043737; PubMed=10984043;			
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kovalek D.J., Lagrou M., RA Garber R.L., Goltier S.N., Folger K.R., Kas A., Marbig K., Yuan Y., RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Marbig K., Lim R.M., RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;			

Search completed: August 9, 2003, 16:32:55
Job time : 51.0429 secs